

RAW SEQUENCE LISTING

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Application Serial Number: 10/534583
Source: PCT
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PATENT APPLICATION: US/10/534,583

DATE: 05/19/2005

TIME: 10:23:30

Input Set : A:\235670.ST25 - US Sequence Listing.txt
 Output Set: N:\CRF4\05182005\J534583.raw

3 <110> APPLICANT: KISHIMOTO, Takahide
 4 SOGABE, Atsushi
 5 OKA, Masanori
 7 <120> TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS FOR PRODUCING THE SAME

AND

8 REAGENT COMPOSITION USING THE SAME
 10 <130> FILE REFERENCE: 235670
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/534,583
 C--> 12 <141> CURRENT FILING DATE: 2005-05-11
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/014423
 13 <151> PRIOR FILING DATE: 2003-11-13
 15 <150> PRIOR APPLICATION NUMBER: JP2002-329427
 16 <151> PRIOR FILING DATE: 2002-11-13
 18 <150> PRIOR APPLICATION NUMBER: JP2002-329428
 19 <151> PRIOR FILING DATE: 2002-11-13
 21 <150> PRIOR APPLICATION NUMBER: JP2003-33641
 22 <151> PRIOR FILING DATE: 2003-02-12
 25 <160> NUMBER OF SEQ ID NOS: 14
 27 <170> SOFTWARE: PatentIn version 3.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 389
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Arthrobacter SP. TE1826
 34 <400> SEQUENCE: 1
 36 Met Ser Ile Lys Lys Asp Tyr Asp Val Ile Val Val Gly Ala Gly Ser
 37 1 5 10 15
 40 Met Gly Met Ala Ala Gly Tyr Tyr Leu Ser Lys Gln Gly Val Lys Thr
 41 20 25 30
 44 Leu Leu Val Asp Ser Phe His Pro Pro His Thr Asn Gly Ser His His
 45 35 40 45
 48 Gly Asp Thr Arg Ile Ile Arg His Ala Tyr Gly Glu Gly Arg Glu Tyr
 49 50 55 60
 52 Val Pro Phe Ala Leu Arg Ala Gln Glu Leu Trp Tyr Glu Leu Glu Lys
 53 65 70 75 80
 56 Glu Thr His His Lys Ile Phe Thr Lys Thr Gly Val Leu Val Phe Gly
 57 85 90 95
 60 Pro Lys Gly Glu Ala Pro Phe Val Ala Glu Thr Met Glu Ala Ala Lys
 61 100 105 110
 64 Glu His Ser Leu Asp Val Asp Leu Leu Glu Gly Ser Glu Ile Asn Lys
 65 115 120 125
 68 Arg Trp Pro Gly Val Thr Val Pro Glu Asn Tyr Asn Ala Ile Phe Glu
 69 130 135 140
 72 Lys Asn Ser Gly Val Leu Phe Ser Glu Asn Cys Ile Arg Ala Tyr Arg
 73 145 150 155 160

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76 Glu Leu Ala Glu Ala Asn Gly Ala Lys Val Leu Thr Tyr Thr Pro Val
 77 165 170 175
 80 Glu Asp Phe Glu Ile Ala Glu Asp Phe Val Lys Ile Gln Thr Ala Tyr
 81 180 185 190
 84 Gly Ser Phe Thr Ala Ser Lys Leu Ile Val Ser Met Gly Ala Trp Asn
 85 195 200 205
 88 Ser Lys Leu Leu Ser Lys Leu Asn Ile Glu Ile Pro Leu Gln Pro Tyr
 89 210 215 220
 92 Arg Gln Val Val Gly Phe Phe Glu Cys Asp Glu Lys Lys Tyr Ser Asn
 93 225 230 235 240
 96 Thr His Gly Tyr Pro Ala Phe Met Val Glu Val Pro Thr Gly Ile Tyr
 97 245 250 255
 100 Tyr Gly Phe Pro Ser Phe Gly Gly Cys Gly Leu Lys Ile Gly Tyr His
 101 260 265 270
 104 Thr Tyr Gly Gln Lys Ile Asp Pro Asp Thr Ile Asn Arg Glu Phe Gly
 105 275 280 285
 108 Ile Tyr Pro Glu Asp Glu Gly Asn Ile Arg Lys Phe Leu Glu Thr Tyr
 109 290 295 300
 112 Met Pro Gly Ala Thr Gly Glu Leu Lys Ser Gly Ala Val Cys Met Tyr
 113 305 310 315 320
 116 Thr Lys Thr Pro Asp Glu His Phe Val Ile Asp Leu His Pro Gln Phe
 117 325 330 335
 120 Ser Asn Val Ala Ile Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe
 121 340 345 350
 124 Ser Ser Val Val Gly Glu Thr Leu Ser Gln Leu Ala Val Thr Gly Lys
 125 355 360 365
 128 Thr Glu His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys
 129 370 375 380
 132 Gln Lys Glu Thr Ile
 133 385
 136 <210> SEQ ID NO: 2
 137 <211> LENGTH: 1167
 138 <212> TYPE: DNA
 139 <213> ORGANISM: Arthrobacter SP. TE1826
 141 <220> FEATURE:
 142 <221> NAME/KEY: CDS
 143 <222> LOCATION: (1)..(1167)
 144 <223> OTHER INFORMATION:
 W--> 146 <400> 2

147 atg agt att aaa aaa gat tat gat gta att gtg gtt ggc gct ggt tcc 48
 148 Met Ser Ile Lys Lys Asp Tyr Asp Val Ile Val Val Gly Ala Gly Ser
 149 1 5 10 15
 151 atg gga atg gca gct ggg tac tat ctg tct aaa caa ggt gtt aaa aca 96
 152 Met Gly Met Ala Ala Gly Tyr Tyr Leu Ser Lys Gln Gly Val Lys Thr
 153 20 25 30
 155 cta ttg gta gat tca ttt cat cct ccc cat aca aat ggc agc cat cat 144
 156 Leu Leu Val Asp Ser Phe His Pro Pro His Thr Asn Gly Ser His His
 157 35 40 45
 159 ggc gat aca cgg atc att cgt cac gca tat ggc gaa gga aga gag tat 192

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160	Gly	Asp	Thr	Arg	Ile	Ile	Arg	His	Ala	Tyr	Gly	Glu	Gly	Arg	Glu	Tyr	
161	50					55					60						
163	gta	ccg	ttt	gcc	ttg	aga	gca	caa	gag	tta	tgg	tat	gaa	tta	gaa	aag	240
164	Val	Pro	Phe	Ala	Leu	Arg	Ala	Gln	Glu	Leu	Trp	Tyr	Glu	Leu	Glu	Lys	
165	65					70					75					80	
167	gag	act	cat	cat	aaa	ata	ttt	aca	aaa	aca	ggt	gta	ctc	gtt	ttt	ggt	288
168	Glu	Thr	His	His	Lys	Ile	Phe	Thr	Lys	Thr	Gly	Val	Leu	Val	Phe	Gly	
169					85					90					95		
171	cct	aaa	gga	gaa	gct	cct	ttc	gtt	gcc	gaa	aca	atg	gaa	gcc	gca	aag	336
172	Pro	Lys	Gly	Glu	Ala	Pro	Phe	Val	Ala	Glu	Thr	Met	Glu	Ala	Ala	Lys	
173					100					105					110		
175	gaa	cat	tca	tta	gat	gtt	gat	tta	cta	gaa	gga	agt	gaa	ata	aat	aag	384
176	Glu	His	Ser	Leu	Asp	Val	Asp	Leu	Leu	Glu	Gly	Ser	Glu	Ile	Asn	Lys	
177					115					120					125		
179	cgt	tgg	cca	ggt	gta	acg	gtt	cct	gag	aat	tat	aat	gct	att	ttt	gaa	432
180	Arg	Trp	Pro	Gly	Val	Thr	Val	Pro	Glu	Asn	Tyr	Asn	Ala	Ile	Phe	Glu	
181					130					135					140		
183	aaa	aat	tct	ggt	gtc	tta	ttt	agt	gaa	aat	tgt	att	cgc	gct	tac	cgt	480
184	Lys	Asn	Ser	Gly	Val	Leu	Phe	Ser	Glu	Asn	Cys	Ile	Arg	Ala	Tyr	Arg	
185					145					150					155		
187	gaa	ttg	gcg	gaa	gca	aat	ggt	gcg	aaa	gtt	cta	acg	tac	aca	ccc	gtt	528
188	Glu	Leu	Ala	Glu	Ala	Asn	Gly	Ala	Lys	Val	Leu	Thr	Tyr	Thr	Pro	Val	
189					165					170					175		
191	gaa	gat	ttc	gag	att	gcc	gag	gac	ttc	gtc	aaa	atc	caa	acc	gcc	tat	576
192	Glu	Asp	Phe	Glu	Ile	Ala	Glu	Asp	Phe	Val	Lys	Ile	Gln	Thr	Ala	Tyr	
193					180					185					190		
195	ggc	tcc	ttt	aca	gcc	agt	aaa	tta	att	gtt	agc	atg	ggc	gct	tgg	aat	624
196	Gly	Ser	Phe	Thr	Ala	Ser	Lys	Leu	Ile	Val	Ser	Met	Gly	Ala	Trp	Asn	
197					195					200					205		
199	agc	aaa	ctg	cta	tca	aaa	tta	aat	att	gaa	atc	cca	ttg	cag	cca	tac	672
200	Ser	Lys	Leu	Ser	Lys	Leu	Asn	Ile	Glu	Ile	Pro	Leu	Gln	Pro	Tyr		
201					210					215					220		
203	cgt	caa	gtt	gtc	gga	ttc	ttc	gaa	tgt	gat	gaa	aaa	aaa	tat	agc	aat	720
204	Arg	Gln	Val	Val	Gly	Phe	Phe	Glu	Cys	Asp	Glu	Lys	Lys	Tyr	Ser	Asn	
205					225					230					235		
207	aca	cat	ggt	tat	ccg	gcg	ttc	atg	gtc	gaa	gtc	cca	act	ggc	atc	tat	768
208	Thr	His	Gly	Tyr	Pro	Ala	Phe	Met	Val	Glu	Val	Pro	Thr	Gly	Ile	Tyr	
209					245					250					255		
211	tac	gga	ttt	cca	agc	ttc	ggc	ggc	tgc	ggc	ttg	aaa	ata	ggc	tat	cat	816
212	Tyr	Gly	Phe	Pro	Ser	Phe	Gly	Gly	Cys	Gly	Leu	Lys	Ile	Gly	Tyr	His	
213					260					265					270		
215	acg	tat	ggt	caa	aaa	atc	gat	cca	gat	acg	att	aat	cgt	gaa	ttt	ggt	864
216	Thr	Tyr	Gly	Gln	Lys	Ile	Asp	Pro	Asp	Thr	Ile	Asn	Arg	Glu	Phe	Gly	
217					275					280					285		
219	att	tac	ccg	gag	gat	gaa	ggg	aat	att	cgc	aaa	ttc	ctg	gaa	aca	tat	912
220	Ile	Tyr	Pro	Glu	Asp	Glu	Gly	Asn	Ile	Arg	Lys	Phe	Leu	Glu	Thr	Tyr	
221					290					295					300		
223	atg	ccg	gga	gca	acc	ggc	gaa	tta	aaa	agt	ggg	gca	gtt	tgc	atg	tac	960
224	Met	Pro	Gly	Ala	Thr	Gly	Glu	Leu	Lys	Ser	Gly	Ala	Val	Cys	Met	Tyr	

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225	305	310	315	320	
227	aca aaa aca cct gat gag cat ttc gtg att gat tta cat cct caa ttc				1008
228	Thr Lys Thr Pro Asp Glu His Phe Val Ile Asp Leu His Pro Gln Phe				
229	325	330	335		
231	tcg aat gtc gcg att gca gcc gga ttc tcc gga cat ggg ttt aaa ttc				1056
232	Ser Asn Val Ala Ile Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe				
233	340	345	350		
235	tca agc gta gtt ggt gaa aca tta agt caa tta gct gta acc ggt aaa				1104
236	Ser Ser Val Val Gly Glu Thr Leu Ser Gln Leu Ala Val Thr Gly Lys				
237	355	360	365		
239	aca gaa cac gat att tcc atc ttt tca atc aat cgc cct gct tta aaa				1152
240	Thr Glu His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys				
241	370	375	380		
243	caa aaa gaa acg att				1167
244	Gln Lys Glu Thr Ile				
245	385				
248	<210> SEQ ID NO: 3				
249	<211> LENGTH: 38				
250	<212> TYPE: DNA				
251	<213> ORGANISM: Artificial Sequence				
253	<220> FEATURE:				
254	<223> OTHER INFORMATION: Arthrobacter SP. TE1826				
256	<400> SEQUENCE: 3				
257	gactcatcat aaaatattta caagaacagg tgtactcg				38
260	<210> SEQ ID NO: 4				
261	<211> LENGTH: 36				
262	<212> TYPE: DNA				
263	<213> ORGANISM: Artificial Sequence				
265	<220> FEATURE:				
266	<223> OTHER INFORMATION: Arthrobacter SP. TE1826				
268	<400> SEQUENCE: 4				
269	gtgtcttatt tagtggaaat attattcgcg cttacc				36
272	<210> SEQ ID NO: 5				
273	<211> LENGTH: 36				
274	<212> TYPE: DNA				
275	<213> ORGANISM: Artificial Sequence				
277	<220> FEATURE:				
278	<223> OTHER INFORMATION: Arthrobacter SP. TE1826				
280	<400> SEQUENCE: 5				
281	gaattggcg aagcaaaagg tgcgaaagt ctaacg				36
284	<210> SEQ ID NO: 6				
285	<211> LENGTH: 38				
286	<212> TYPE: DNA				
287	<213> ORGANISM: Artificial Sequence				
289	<220> FEATURE:				
290	<223> OTHER INFORMATION: Arthrobacter SP. TE1826				
292	<400> SEQUENCE: 6				
293	gccagtaaat taattgttag cgccggcgct tgaaatag				38
296	<210> SEQ ID NO: 7				

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297 <211> LENGTH: 38
 298 <212> TYPE: DNA
 299 <213> ORGANISM: Artificial Sequence
 301 <220> FEATURE:
 302 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
 304 <400> SEQUENCE: 7
 305 gaatagcaaa ctgctaccaa aattaaatat tgaaatcc 38
 308 <210> SEQ ID NO: 8
 309 <211> LENGTH: 36
 310 <212> TYPE: DNA
 311 <213> ORGANISM: Artificial Sequence
 313 <220> FEATURE:
 314 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
 316 <400> SEQUENCE: 8
 317 gtcggattct tcgaaagcga tgaaaaaaaaa tatagc 36
 320 <210> SEQ ID NO: 9
 321 <211> LENGTH: 38
 322 <212> TYPE: DNA
 323 <213> ORGANISM: Artificial Sequence
 325 <220> FEATURE:
 326 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
 328 <400> SEQUENCE: 9
 329 gtgatgaaaaaaa aaaaatatagc tatacacatg gttatccg 38
 332 <210> SEQ ID NO: 10
 333 <211> LENGTH: 33
 334 <212> TYPE: DNA
 335 <213> ORGANISM: Artificial Sequence
 337 <220> FEATURE:
 338 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
 340 <400> SEQUENCE: 10
 341 ccggcgttca tggtccaggt cccaaactggc atc 33
 344 <210> SEQ ID NO: 11
 345 <211> LENGTH: 37
 346 <212> TYPE: DNA
 347 <213> ORGANISM: Artificial Sequence
 349 <220> FEATURE:
 350 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
 352 <400> SEQUENCE: 11
 353 gaaacattaa gtcaattagt tgtaaccggt aaaacag 37
 356 <210> SEQ ID NO: 12
 357 <211> LENGTH: 36
 358 <212> TYPE: DNA
 359 <213> ORGANISM: Artificial Sequence
 361 <220> FEATURE:
 362 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
 364 <400> SEQUENCE: 12
 365 caaaaacagg tgtactcggt tttggtccta aaggag 36
 368 <210> SEQ ID NO: 13
 369 <211> LENGTH: 37

VERIFICATION SUMMARY

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Input Set : A:\235670.ST25 - US Sequence Listing.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:146 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:144